

**FIGURE 1**

GGGGGAGAAGGCGGCCGAGCCCCAGCTCTCCGAGCACCGGGTCGGAAGCCGCGACCCGAGCCGCGCAGGAA  
GCTGGGACCGGAACCTCGGCGGACCCGGCCCCACCCAACCTCACCTGCGCAGGTACACAGCACCCCTCGGAAC  
CCAGAGGCCCCGCGCTCTGAAGGTGACCCCCCTGGGGAGGAAGGCGATGGCCCCCTGCGAGGACGATGGCCCC  
CGCCCCGCTCGCCCCGGCCGGCATCCCTGCCGTGCGCTTGTGGCTTCTGTGCACGCTCGGCCCTCCAGGGCA  
CCCAGGCCGGGCCACCGCCCGCCCCCTGGGCTGCCCGCGGGAGCCGACTGCCTGAACAGCTTTACCGCC  
GGGGTGCTTGCTTCGTGCTGGACACCAACGCCTCGGTGAGCAACGGAGCTACCTTCTGGAGTCCCCCAC  
CGTGCGCCGGGGCTGGGACTGCGTGCGCGCTGCTGCACCAACCCAGAACTGCAACTTGGCGCTAGTGGAGC  
TGCAGCCCCGACCGCGGGGAGGACGCCATCGCCGCGCTGCTTCTCATCAACTGCCTCTACGAGCAGAACTTC  
GTGTGCAAGTTTCGCGCCCAGGGAGGGCTTCATCAACTACCTCACGAGGGAAGTGTACCGCTCCTACCGCCA  
GCTGCGGACCCAGGGCTTTGGAGGGTCTGGGATCCCCAAGGCCTGGGCAGGCATAGACTTGAAGGTACAAC  
CCCAGGAACCCCTGGTGCTGAAGGATGTGGAAAACACAGATTGGCGCCTACTGCGGGGTGACACGGATGTC  
AGGGTAGAGAGGAAAGACCCAAACCAGGTGGAAGTGTGGGGACTCAAGGAAGGCACCTACCTGTTCCAGCT  
GACAGTGAAGTACTGCTCAGACACCCAGAGGACACGGCCAACGTACAGTCACTGTGCTGTCCACCAAGCAGA  
CAGAAGACTACTGCCTCGCATCCAACAAGGTGGGTGCGTGCCGGGGCTCTTTCCACGCTGGTACTATGAC  
CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAACCTACCTTCGGGA  
AGAAGAGTGCATTCTAGCCTGTGCGGGTGTGCAAGGTGGGCCTTTGAGAGGCAGCTCTGGGGCTCAGGCGA  
CTTTCCCCCAGGGCCCCCTCCATGGAAAGGCGCCATCCAGTGTGCTCTGGCACCTGTGAGCCCAACCACTTC  
CGCTGCAGCAATGGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCCTC  
CGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACA  
AAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTACAACCCC  
TTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAACAACCTTTGAGGAAGAGCA  
GCAGTGCCTCGAGTCTTGTGCGGGCATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCATTC  
CCAGCACAGGCTCTGTGGAGATGGCTGTACAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATC  
TTGGGTTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCCACGGACACCACCACCACCACCACCACCACC  
TGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACACCACCCGGCCCCCTCT  
GAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTTGCCAAGGCAGAGGCCTGGGCTGGGAAA  
AACTTTGGAACCAAGACTCTTGCTGTTTCCCAGGCCCCACTGTGCTCAGAGACCAGGGCTCCAGCCCCCTCT  
TGGAGAAGTCTCAGCTAAGCTCACGTCTGAGAAAGCTCAAAGGTTTGAAGGAGCAGAAAACCCCTGGGC  
CAGAAGTACCAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTT  
CAAAGCTGCCTGTCCCTACCCCATGGTGCTAGGAAGAGGAGTGGGGTGGTGTGACACCCTGGAGGCCCCAA  
CCCTGTCTCTCCGAGCTCCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGGACTTCCCTGTGTAGTTT  
GTGCTGTAAAGAGTTGCTTTTTGTTTATTTAATGCTGTGGCATGGGTGAAGAGGAGGGGAAGAGGCCTGTT  
TGGCCTCTCTGTCTCTCTTCTCTTCCCCAAGATTGAGCTCTCTGCCCTTGATCAGCCCCACCCCTGGCC  
TAGACCAGCAGACAGAGCCAGGAGAGGCTCAGCTGCATTCCGCAGCCCCCACCCTCAAGGTTCTCCAACAT  
CACAGCCCAGCCCACCCACTGGGTAATAAAAGTGGTTTGTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 2**

MAPARTMARARLAPAGIPAVALWLLCTLGLQGTQAGPPPAPPGLPAGADCLNSFTAGVPGFVLDTNASVSN  
 GATFLESPTVRRGWDCVRACCTTQNCNLALVELQPDREGDAIAACFLINCLYEQNFVCKFAPREGFINYL  
 REVYRSYRQLRTQGFGGSGIPKAWAGIDLKVQPQEPLVLKDVENTDWRLLRGDDVRVERKDPNQVELWGL  
 KEGTYLFLQTLVTSSDHPEDTANVTVTVLSTKQTEDYCLASNKVGRCRGSFPRWYYDPTEQICKSFVYGGCL  
 GNKNYYLREEECILACRGVQGGPLRGSSGAQATFPQGSPMERRHPVCSGTCQPTQFRCSNGCCIDSFLECD  
 DTPNCPDASDEAAACEKYTSGFDELQRIHFPSDKGHCVDL PDTGLCKESI PRWYYPFSEHCAREFTYGGCYG  
 NKNNFEEEQQCLESRCGISKKDVFLRREIPI PSTGSVEMAVTVFLVICIVVVVAILGYCFFKNQRKDFHG  
 HHHHPPTPASSTVSTTEDTEHLVYNHTTRPL

signal sequence:	Amino acids 1-35
transmembrane domain:	Amino acids 466-483
N-glycosylation sites:	Amino acids 66-70;235-239;523-527.
N-myristoylation sites:	Amino acids 29-35;43-49;161-167; 212-218;281-287;282-288; 285-291;310-316;313-319; 422-428;423-429;426-432
Cell attachment sequence:	Amino acids 193-199
Pancreatic trypsin inhibitor (Kunitz) family signatures:	Amino acids 278-298;419-438

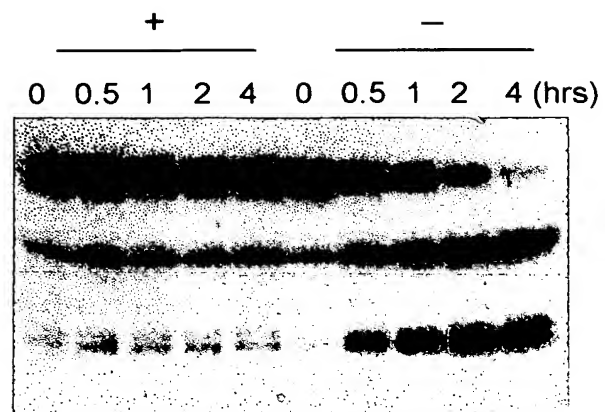


FIG. 3(a)

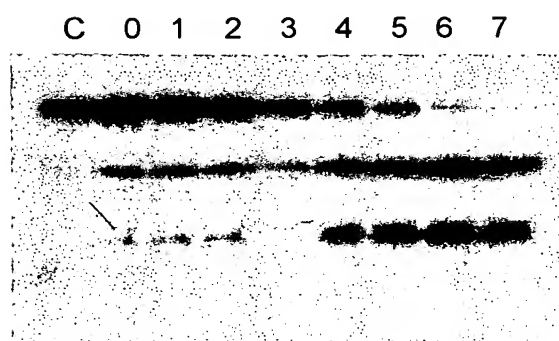


FIG. 3(b)

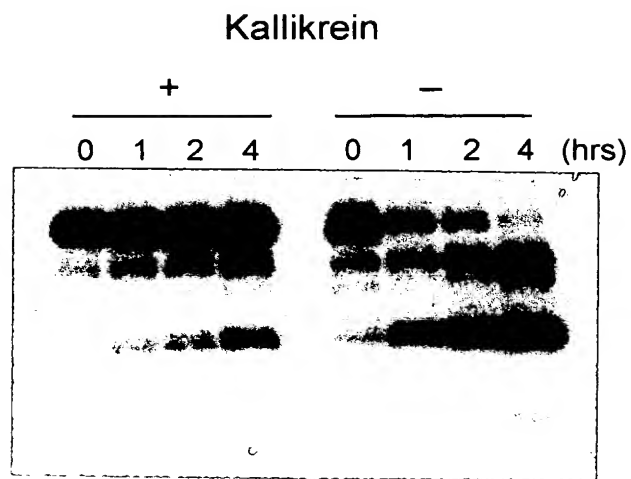


FIG. 4(a)

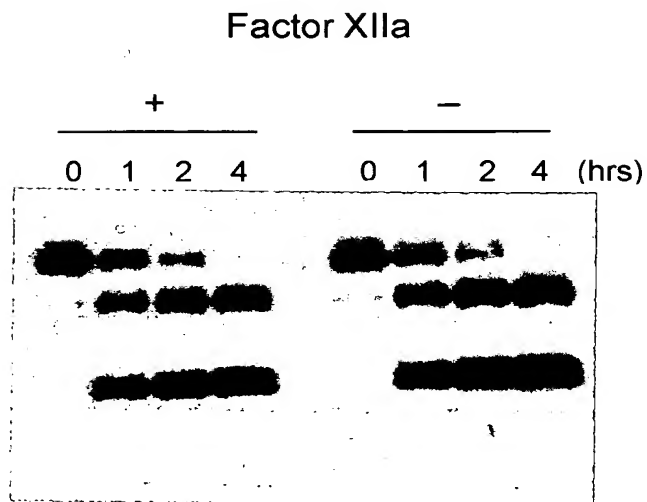
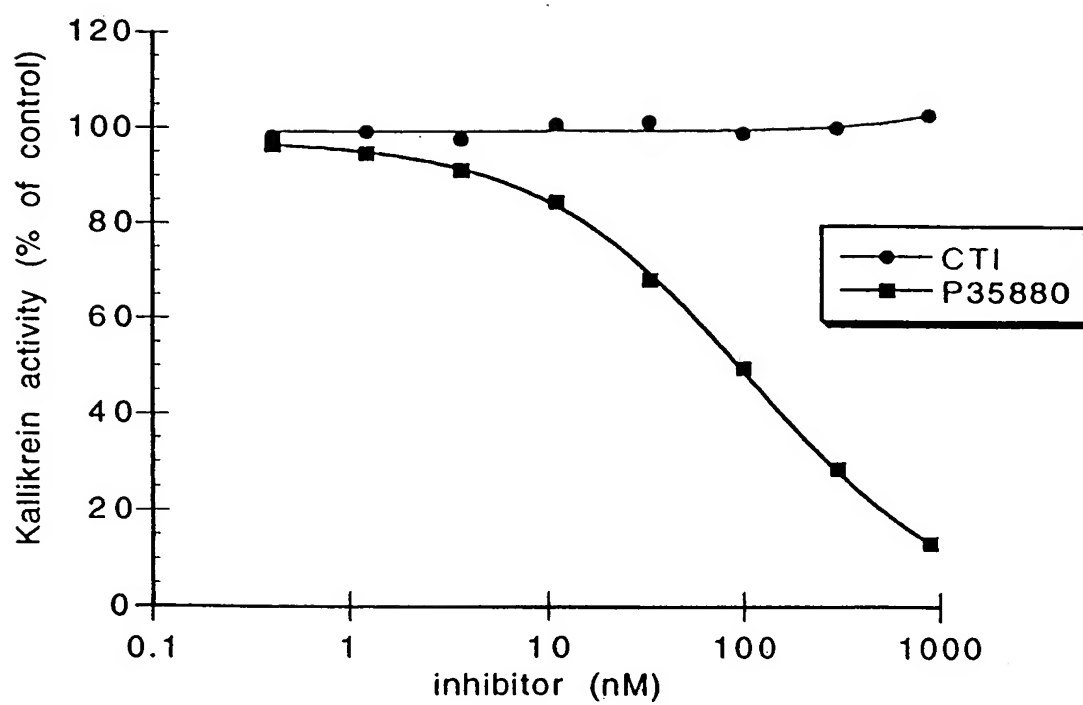


FIG. 4(b)



**FIG. 5**